Appendix A

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 10, 2003, 14:38:55 ; Search time 13.4774 Seconds
                 (without alignments)
                 692.052 Million cell updates/sec

Title: US-08-880-855-39
Perfect score: 1685
Sequence: 1 MRRASRDYTKYLRGSEEMGG.........LLDPDQDATYFGAFKVRDID 317

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1685	100.0	317	3		Sequence 13, App
2	1685	100.0	317	4		Sequence 13, App
3	1685	100.0	317	4		Sequence 13, App
4	1685	100.0	317	4		Sequence 13, App
5	1685	100.0	317	4	US-09-577-780-13	Sequence 13, App

Appendix A

RESULT 5
US-09-577-780-13
Sequence 13, Application US/09577780
Patent No. 6419929
GENERAL INFORMATION:
    APPLICANT: Anderson, Dirk M.
        Galibert, Laurent
        Maraskovsky, Eugene
    TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
    NUMBER OF SEQUENCES: 19
    CORRESPONDENCE ADDRESS:
        ADDRESSEE: Immunex Corporation, Law Department
        STREET: 51 University Street
        CITY: Seattle
        STATE: WA
        COUNTRY: USA
        ZIP: 98101
    COMPUTER READABLE FORM:
        MEDIUM TYPE: Floppy disk
        COMPUTER: Apple Power Macintosh
        OPERATING SYSTEM: Apple Operating System 7.5.5
        SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
    CURRENT APPLICATION DATA:
        APPLICATION NUMBER: US/09/577,780
        FILING DATE: 24-May-2000
        CLASSIFICATION: <Unknown>
    PRIOR APPLICATION DATA:
        APPLICATION NUMBER: 08/995,659
        FILING DATE: <Unknown>
        APPLICATION NUMBER: USSN 08/813,509
        FILING DATE: 07 MARCH 1997
        APPLICATION NUMBER: USSN 08/772,330
        FILING DATE: 23 DECEMBER 1996
    ATTORNEY/AGENT INFORMATION:
        NAME: Perkins, Patricia Anne
        REGISTRATION NUMBER: 34,693
        REFERENCE/DOCKET NUMBER: 2852-A
    TELECOMMUNICATION INFORMATION:
        TELEPHONE: (206)587-0430
        TELEFAX: (206)233-0644
    INFORMATION FOR SEQ ID NO: 13:
        SEQUENCE CHARACTERISTICS:
        LENGTH: 317 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
        MOLECULE TYPE: protein
        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-577-780-13

Query Match   100.0%;   Score 1685;   DB 4;   Length 317;
Best Local Similarity 100.0%;   Pred. No. 1.4e-163;
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYTKYLRGSEEMGGGPGAPHEGPLHAPPPPAPHQPPAASRSMFVALLGLGLGQV 60

Qy   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VCSVALFFYFRAQMDPNRISEDGTHCIYRILRLHENADFQDTTLESQDTKLIPDSCRRIK 120

Qy   121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 QAFQGAVQKELQHIVGSQHIRAEKAMVDGSWLDLAKRSKLEAQPFAHLTINATDIPSGSH 180

Qy   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 KVSLSSWYHDRGWAKISNMTFSNGKLIVNQDGFYYLYANICFRHHETSGDLATEYLQLMV 240

Qy   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 YVTKTSIKIPSSHTLMKGGSTKYWSGNSEFHFYSINVGGFFKLRSGEEISIEVSNPSLLD 300

Qy   301 PDQDATYFGAFKVRDID 317
           |||||||||||||||||
Db   301 PDQDATYFGAFKVRDID 317

OM protein - protein search, using sw model

GenCore version 5.1.4_p5_4578
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Run on: March 10, 2003, 14:38:55 ; Search time 13.4349 Seconds
                  (without alignments)
                  692.052 Million cell updates/sec

Title: US-08-880-855-37
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS..........LLDPDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB ID	Description
1	1675	100.0	316	US-08-880-855-37	
2	1675	100.0	316	US-08-989-362-2	Sequence 2, Appli

ALIGNMENTS

Appendix B

us-08-880-855-37.rai

```
Qy  181  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVYPTDYLLQLMVY  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVYPTDYLLQLMVY  240

Qy  241  VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP  300

Qy  301  DQDATYFGAFKVQDID  316
         ||||||||||||||||
Db  301  DQDATYFGAFKVQDID  316
```

RESULT 2
US-08-989-362-2

; Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: DNAX Research Institute
;   STREET: 901 California Avenue
;   CITY: Palo Alto
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94304-1104
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/989,362
;   FILING DATE: 12-DEC-1997
;   CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/032,846
;   FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
;   NAME: Ching, Edwin P.
;   REGISTRATION NUMBER: 34,090
;   REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (650)852-9196
;   TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 316 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-989-362-2

Query Match   100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity   100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy    1  MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALLGLGLGQ  60

Qy   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQODSTLESEDTLPDSCRRMKQ  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  VVCSIALFLYFRAQMDPNRISEDSTHCFYRILRLHENAGLQODSTLESEDTLPDSCRRMKQ  120

Qy  121  AFQGAVQKELQHIVGPQRFSGAPAVMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  AFQGAVQKELQHIVGPQRFSGAPAVMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHK  180
```

Appendix B

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run On: March 10, 2003, 14:38:55 ; Search time 13.4349 Seconds
                                                 (without alignments)
                                                 692.052 Million cell updates/sec

Title: US-08-880-855-37
Perfect score: 1675
Sequence: 1 MRRASRDYGKYLRSSEEMGS............LLDPDQDATYFGAFKVQDID 316

Scoring table: BLOSUM62
                       Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
              1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
              2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
              3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
              4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
              5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

              Pred. No. is the number of results predicted by chance to have a
              score greater than or equal to the score of the result being printed,
              and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result   %   Query
No.   Score Match Length DB   ID   Description

 1   1675   100.0   316   4   US-08-989-362-2   Sequence 2, Appli
 2   1675   100.0   316

ALIGNMENTS

Appendix B

us-08-880-855-37.rai

RESULT 2
US-08-989-362-2

Sequence 2, Application US/08989362
; Patent No. 6242586
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Mattson, Jeanine D.
; TITLE OF INVENTION: Mammalian Cell Surface Antigens; Related
; TITLE OF INVENTION: Reagents
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,362
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 56
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,846
; FILING DATE: 13-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0686
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-989-362-2

Query Match   100.0%; Score 1675; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 4.7e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALIGLGLGLGLGQ 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRRASRDYGKYLRSSEEMGSGPGVPHEGPLHPAPSAPAPAPPPAASRSMFLALIGLGLGQ 60

Qy   61 VVCSIALFLYFRAQMDNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 VVCSIALFLYFRAQMDNRISEDSTHCFYRIRLRHENAGLQDSTLESEDTLPDSCRRMKQ 120

Qy   121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQFFAHLTINAASIPSGSHK 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 AFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQFFAHLTINAASIPSGSHK 180

Qy   181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVY 240

Qy   241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 VVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300

Qy   301 DQDATYFGAFKVQDID 316
          ||||||||||||||||
Db   301 DQDATYFGAFKVQDID 316